

# SEQUENCE LISTING

<110> Han, Hui-Quan  
Kwak, Keith

<120> Human E3 Alpha Ubiquitin Ligase Family

<130> 01017/35966C

<140> To be assigned

<141> Herewith

<150> US 09/724,126

<151> 2000-11-28

<150> US 60/187,911

<151> 1999-03-08

<160> 29

<170> PatentIn Ver. 2.0

<210> 1

<211> 6308

<212> DNA

<213> Homo sapiens

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<221> CDS

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Ser	Val	Gln	Phe	Phe	Thr	Ala	Pro	Thr	Leu	Ala	Arg	Met	Leu	Ile	Thr	
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Asp Pro Ala Phe Gly Phe Pro Lys Leu Glu Gln Ala Asn Lys Pro Ser
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His Leu Cys Gly Arg Val Phe Lys Val Gly Glu Pro Thr Tyr Ser Cys
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Arg Tyr Gly Asp Phe Gln Tyr Cys Glu Gln Ala Lys Ser Val Ile Val
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1

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Ser His Phe Glu His Leu Cys Asn Tyr Leu Ser Leu Pro Thr Asn Leu	
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att cac ctt ttt caa gaa aac agt gac atc atg aac tcc ctg att gaa	5481
Ile His Leu Phe Gln Glu Asn Ser Asp Ile Met Asn Ser Leu Ile Glu	
1560 1565 1570	
agt tgg tgc cag aac agt gaa gtt aaa cgg tat cta aat ggc gag aga	5529
Ser Trp Cys Gln Asn Ser Glu Val Lys Arg Tyr Leu Asn Gly Glu Arg	
1575 1580 1585	
gga gcg ata agc tac ccc aga gga gct aac aaa ctg ata gac ctt cca	5577
Gly Ala Ile Ser Tyr Pro Arg Gly Ala Asn Lys Leu Ile Asp Leu Pro	
1590 1595 1600	
gag gat tac agc agc ctc att aac caa gca tcc aat ttc tgc tgc ccc	5625
Glu Asp Tyr Ser Ser Leu Ile Asn Gln Ala Ser Asn Phe Ser Cys Pro	
1605 1610 1615 1620	
aaa tca ggt ggc gac aag agc aga gct cct act ctg tgc ctc gtg tgt	5673
Lys Ser Gly Gly Asp Lys Ser Arg Ala Pro Thr Leu Cys Leu Val Cys	
1625 1630 1635	
ggg agt ctc ctc tgc tct cag agt tac tgc tgc caa gct gag ctg gag	5721
Gly Ser Leu Leu Cys Ser Gln Ser Tyr Cys Cys Gln Ala Glu Leu Glu	
1640 1645 1650	
ggt gag gac gtc gga gcc tgc aca gca cac acc tac tcc tgc ggc tcc	5769
Gly Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr Ser Cys Gly Ser	
1655 1660 1665	
ggg gcc ggc atc ttc ctg aga gtg cgg gaa tgt cag gtg cta ttt tta	5817
Gly Ala Gly Ile Phe Leu Arg Val Arg Glu Cys Gln Val Leu Phe Leu	
1670 1675 1680	
gct ggc aaa acc aaa gga tgt ttt tat tct cct cct tac ctt gac gac	5865
Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro Tyr Leu Asp Asp	
1685 1690 1695 1700	
tat gga gag acc gac cag gga ctc aga cga gga aat cct tta cat tta	5913
Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn Pro Leu His Leu	
1705 1710 1715	
tgc caa gag cgg ttt cga aag atc cag aag ctc tgg cag cag cat agt	5961
Cys Gln Glu Arg Phe Arg Lys Ile Gln Lys Leu Trp Gln Gln His Ser	
1720 1725 1730	
atc aca gag gag atc gga cac gcg cag gag gct aac cag acc ctg gtc	6009
Ile Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn Gln Thr Leu Val	
1735 1740 1745	
gga att gac tgg cag cat tta taatcgctcc tctactaaaa acttgacttg	6060
Gly Ile Asp Trp Gln His Leu	
1750 1755	
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 <212> PRT  
 <213> Mouse

<400> 6

Met	Ala	Ser	Glu	Met	Glu	Pro	Glu	Val	Gln	Ala	Ile	Asp	Arg	Ser	Leu
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Leu	Glu	Cys	Ser	Ala	Glu	Glu	Ile	Ala	Gly	Arg	Trp	Leu	Gln	Ala	Thr
			20					25					30		
Asp	Leu	Asn	Arg	Glu	Val	Tyr	Gln	His	Leu	Ala	His	Cys	Val	Pro	Lys
		35					40					45			
Ile	Tyr	Cys	Arg	Gly	Pro	Asn	Pro	Phe	Pro	Gln	Lys	Glu	Asp	Thr	Leu
	50					55					60				
Ala	Gln	His	Ile	Leu	Leu	Gly	Pro	Met	Glu	Trp	Tyr	Ile	Cys	Ala	Glu
65					70					75					80
Asp	Pro	Ala	Leu	Gly	Phe	Pro	Lys	Leu	Glu	Gln	Ala	Asn	Lys	Pro	Ser
				85					90					95	
His	Leu	Cys	Gly	Arg	Val	Phe	Lys	Val	Gly	Glu	Pro	Thr	Tyr	Ser	Cys
			100					105					110		
Arg	Asp	Cys	Ala	Val	Asp	Pro	Thr	Cys	Val	Leu	Cys	Met	Glu	Cys	Phe
		115					120					125			
Leu	Gly	Ser	Ile	His	Arg	Asp	His	Arg	Tyr	Arg	Met	Thr	Thr	Ser	Gly
	130					135					140				
Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	Ala	Trp	Lys	Glu	Gly
145					150					155					160
Pro	Tyr	Cys	Gln	Lys	His	Lys	Leu	Ser	Ser	Ser	Glu	Val	Val	Glu	Glu
				165					170					175	
Glu	Asp	Pro	Leu	Val	His	Leu	Ser	Glu	Asp	Val	Ile	Ala	Arg	Thr	Tyr
			180					185					190		
Asn	Ile	Phe	Ala	Ile	Met	Phe	Arg	Tyr	Ala	Val	Asp	Ile	Leu	Thr	Trp
		195					200					205			
Glu	Lys	Glu	Ser	Glu	Leu	Pro	Glu	Asp	Leu	Glu	Val	Ala	Glu	Lys	Ser
	210					215					220				
Asp	Thr	Tyr	Tyr	Cys	Met	Leu	Phe	Asn	Asp	Glu	Val	His	Thr	Tyr	Glu
225					230					235					240
Gln	Val	Ile	Tyr	Thr	Leu	Gln	Lys	Ala	Val	Asn	Cys	Thr	Gln	Lys	Glu
				245					250					255	
Ala	Ile	Gly	Phe	Ala	Thr	Thr	Val	Asp	Arg	Asp	Gly	Arg	Arg	Pro	Val
			260					265					270		
Arg	Tyr	Gly	Asp	Phe	Gln	Tyr	Cys	Asp	Gln	Ala	Lys	Thr	Val	Ile	Val
		275					280					285			
Arg	Asn	Thr	Ser	Arg	Gln	Thr	Lys	Pro	Leu	Lys	Val	Gln	Val	Met	His
	290					295					300				

Ser Ser Val Ala Ala His Gln Asn Phe Gly Leu Lys Ala Leu Ser Trp  
 305 310 315 320  
 Leu Gly Ser Val Ile Gly Tyr Ser Asp Gly Leu Arg Arg Ile Leu Cys  
 325 330 335  
 Gln Val Gly Leu Gln Glu Gly Pro Asp Gly Glu Asn Ser Ser Leu Val  
 340 345 350  
 Asp Arg Leu Met Leu Asn Asp Ser Lys Leu Trp Lys Gly Ala Arg Ser  
 355 360 365  
 Val Tyr His Gln Leu Phe Met Ser Ser Leu Leu Met Asp Leu Lys Tyr  
 370 375 380  
 Lys Lys Leu Phe Ala Leu Arg Phe Ala Lys Asn Tyr Arg Gln Leu Gln  
 385 390 395 400  
 Arg Asp Phe Met Glu Asp Asp His Glu Arg Ala Val Ser Val Thr Ala  
 405 410 415  
 Leu Ser Val Gln Phe Phe Thr Ala Pro Thr Leu Ala Arg Met Leu Leu  
 420 425 430  
 Thr Glu Glu Asn Leu Met Thr Val Ile Ile Lys Ala Phe Met Asp His  
 435 440 445  
 Leu Lys His Arg Asp Ala Gln Gly Arg Phe Gln Phe Glu Arg Tyr Thr  
 450 455 460  
 Ala Leu Gln Ala Phe Lys Phe Arg Arg Val Gln Ser Leu Ile Leu Asp  
 465 470 475 480  
 Leu Lys Tyr Val Leu Ile Ser Lys Pro Thr Glu Trp Ser Asp Glu Leu  
 485 490 495  
 Arg Gln Lys Phe Leu Gln Gly Phe Asp Ala Phe Leu Glu Leu Leu Lys  
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 Cys Met Gln Gly Met Asp Pro Ile Thr Arg Gln Val Gly Gln His Ile  
 515 520 525  
 Glu Met Glu Pro Glu Trp Glu Ala Ala Phe Thr Leu Gln Met Lys Leu  
 530 535 540  
 Thr His Val Ile Ser Met Val Gln Asp Trp Cys Ala Leu Asp Glu Lys  
 545 550 555 560  
 Val Leu Ile Glu Ala Tyr Lys Lys Cys Leu Ala Val Leu Thr Gln Cys  
 565 570 575  
 His Gly Gly Phe Thr Asp Gly Glu Gln Pro Ile Thr Leu Ser Ile Cys  
 580 585 590  
 Gly His Ser Val Glu Thr Ile Arg Tyr Cys Val Ser Gln Glu Lys Val  
 595 600 605  
 Ser Ile His Leu Pro Ile Ser Arg Leu Leu Ala Gly Leu His Val Leu  
 610 615 620  
 Leu Ser Lys Ser Glu Val Ala Tyr Lys Phe Pro Glu Leu Leu Pro Leu  
 625 630 635 640

Ser Glu Leu Ser Pro Pro Met Leu Ile Glu His Pro Leu Arg Cys Leu  
 645 650 655  
 Val Leu Cys Ala Gln Val His Ala Gly Met Trp Arg Arg Asn Gly Phe  
 660 665 670  
 Ser Leu Val Asn Gln Ile Tyr Tyr Tyr His Asn Val Lys Cys Arg Arg  
 675 680 685  
 Glu Met Phe Asp Lys Asp Ile Val Met Leu Gln Thr Gly Val Ser Met  
 690 695 700  
 Met Asp Pro Asn His Phe Leu Met Ile Met Leu Ser Arg Phe Glu Leu  
 705 710 715 720  
 Tyr Gln Leu Phe Ser Thr Pro Asp Tyr Gly Lys Arg Phe Ser Ser Glu  
 725 730 735  
 Val Thr His Lys Asp Val Val Gln Gln Asn Asn Thr Leu Ile Glu Glu  
 740 745 750  
 Met Leu Tyr Leu Ile Ile Met Leu Val Gly Glu Arg Phe Asn Pro Gly  
 755 760 765  
 Val Gly Gln Val Ala Ala Thr Asp Glu Ile Lys Arg Glu Ile Ile His  
 770 775 780  
 Gln Leu Ser Ile Lys Pro Met Ala His Ser Glu Leu Val Lys Ser Leu  
 785 790 795 800  
 Pro Glu Asp Glu Asn Lys Glu Thr Gly Met Glu Ser Val Ile Glu Ser  
 805 810 815  
 Val Ala His Phe Lys Lys Pro Gly Leu Thr Gly Arg Gly Met Tyr Glu  
 820 825 830  
 Leu Lys Pro Glu Cys Ala Lys Glu Phe Asn Leu Tyr Phe Tyr His Phe  
 835 840 845  
 Ser Arg Ala Glu Gln Ser Lys Ala Glu Glu Ala Gln Arg Lys Leu Lys  
 850 855 860  
 Arg Glu Asn Lys Glu Asp Thr Ala Leu Pro Pro Pro Ala Leu Pro Pro  
 865 870 875 880  
 Phe Cys Pro Leu Phe Ala Ser Leu Val Asn Ile Leu Gln Cys Asp Val  
 885 890 895  
 Met Leu Tyr Ile Met Gly Thr Ile Leu Gln Trp Ala Val Glu His His  
 900 905 910  
 Gly Ser Ala Trp Ser Glu Ser Met Leu Gln Arg Val Leu His Leu Ile  
 915 920 925  
 Gly Met Ala Leu Gln Glu Glu Lys His His Leu Glu Asn Ala Val Glu  
 930 935 940  
 Gly His Val Gln Thr Phe Thr Phe Thr Gln Lys Ile Ser Lys Pro Gly  
 945 950 955 960  
 Asp Ala Pro His Asn Ser Pro Ser Ile Leu Ala Met Leu Glu Thr Leu  
 965 970 975

Gln Asn Ala Pro Ser Leu Glu Ala His Lys Asp Met Ile Arg Trp Leu  
 980 985 990  
 Leu Lys Met Phe Asn Ala Ile Lys Lys Ile Arg Glu Cys Ser Ser Ser  
 995 1000 1005  
 Ser Pro Val Ala Glu Ala Glu Gly Thr Ile Met Glu Glu Ser Ser Arg  
 1010 1015 1020  
 Asp Lys Asp Lys Ala Glu Arg Lys Arg Lys Ala Glu Ile Ala Arg Leu  
 025 1030 1035 1040  
 Arg Arg Glu Lys Ile Met Ala Gln Met Ser Glu Met Gln Arg His Phe  
 1045 1050 1055  
 Ile Asp Glu Asn Lys Glu Leu Phe Gln Gln Thr Leu Glu Leu Asp Thr  
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 Ser Ala Ser Ala Thr Leu Asp Ser Ser Pro Pro Val Ser Asp Ala Ala  
 1075 1080 1085  
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 1090 1095 1100  
 Phe Val Thr Cys Ile Leu Cys Gln Glu Glu Gln Glu Val Thr Val Gly  
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 Ser Arg Ala Met Val Leu Ala Ala Phe Val Gln Arg Ser Thr Val Leu  
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 Ser Lys Asp Arg Thr Lys Thr Ile Ala Asp Pro Glu Lys Tyr Asp Pro  
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 Leu Phe Met His Pro Asp Leu Ser Cys Gly Thr His Thr Gly Ser Cys  
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 Gly His Val Met His Ala His Cys Trp Gln Arg Tyr Phe Asp Ser Val  
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 Gln Ala Lys Glu Gln Arg Arg Gln Gln Arg Leu Arg Leu His Thr Ser  
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 Tyr Asp Val Glu Asn Gly Glu Phe Leu Cys Pro Leu Cys Glu Cys Leu  
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 1235 1240 1245  
 Ala Val Thr Gln Gln Ile Lys Val Val Gln Met Leu Arg Arg Lys His  
 1250 1255 1260  
 Asn Ala Ala Asp Thr Ser Ser Ser Glu Asp Thr Glu Ala Met Asn Ile  
 265 1270 1275 1280  
 Ile Pro Ile Pro Glu Gly Phe Arg Pro Asp Phe Tyr Pro Arg Asn Pro  
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 Tyr Ser Asp Ser Ile Lys Glu Met Leu Thr Thr Phe Gly Thr Ala Ala  
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Tyr Lys Val Gly Leu Lys Val His Pro Asn Glu Gly Asp Pro Arg Val  
 1315 1320 1325  
 Pro Ile Leu Cys Trp Gly Thr Cys Ala Tyr Thr Ile Gln Ser Ile Glu  
 1330 1335 1340  
 Arg Ile Leu Ser Asp Glu Glu Lys Pro Val Phe Gly Pro Leu Pro Cys  
 345 1350 1355 1360  
 Arg Leu Asp Asp Cys Leu Arg Ser Leu Thr Arg Phe Ala Ala Ala His  
 1365 1370 1375  
 Trp Thr Val Ala Leu Leu Pro Val Val Gln Gly His Phe Cys Lys Leu  
 1380 1385 1390  
 Phe Ala Ser Leu Val Pro Ser Asp Ser Tyr Glu Asp Leu Pro Cys Ile  
 1395 1400 1405  
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 Pro Ala Leu Gln Cys Gln Asp Phe Ser Gly Ser Ser Leu Ala Thr Gly  
 425 1430 1435 1440  
 Asp Leu His Ile Phe His Leu Val Thr Met Ala His Ile Val Gln Ile  
 1445 1450 1455  
 Leu Leu Thr Ser Cys Thr Glu Glu Asn Gly Met Asp Gln Glu Asn Pro  
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 Thr Gly Glu Glu Glu Leu Ala Ile Leu Ser Leu His Lys Thr Leu His  
 1475 1480 1485  
 Gln Tyr Thr Gly Ser Ala Leu Lys Glu Ala Pro Ser Gly Trp His Leu  
 1490 1495 1500  
 Trp Arg Ser Val Arg Ala Ala Ile Met Pro Phe Leu Lys Cys Ser Ala  
 505 1510 1515 1520  
 Leu Phe Phe His Tyr Leu Asn Gly Val Pro Ala Pro Pro Asp Leu Gln  
 1525 1530 1535  
 Val Ser Gly Thr Ser His Phe Glu His Leu Cys Asn Tyr Leu Ser Leu  
 1540 1545 1550  
 Pro Thr Asn Leu Ile His Leu Phe Gln Glu Asn Ser Asp Ile Met Asn  
 1555 1560 1565  
 Ser Leu Ile Glu Ser Trp Cys Gln Asn Ser Glu Val Lys Arg Tyr Leu  
 1570 1575 1580  
 Asn Gly Glu Arg Gly Ala Ile Ser Tyr Pro Arg Gly Ala Asn Lys Leu  
 585 1590 1595 1600  
 Ile Asp Leu Pro Glu Asp Tyr Ser Ser Leu Ile Asn Gln Ala Ser Asn  
 1605 1610 1615  
 Phe Ser Cys Pro Lys Ser Gly Gly Asp Lys Ser Arg Ala Pro Thr Leu  
 1620 1625 1630  
 Cys Leu Val Cys Gly Ser Leu Leu Cys Ser Gln Ser Tyr Cys Cys Gln  
 1635 1640 1645

Ala Glu Leu Glu Gly Glu Asp Val Gly Ala Cys Thr Ala His Thr Tyr  
1650 1655 1660

Ser Cys Gly Ser Gly Ala Gly Ile Phe Leu Arg Val Arg Glu Cys Gln  
665 1670 1675 1680

Val Leu Phe Leu Ala Gly Lys Thr Lys Gly Cys Phe Tyr Ser Pro Pro  
1685 1690 1695

Tyr Leu Asp Asp Tyr Gly Glu Thr Asp Gln Gly Leu Arg Arg Gly Asn  
1700 1705 1710

Pro Leu His Leu Cys Gln Glu Arg Phe Arg Lys Ile Gln Lys Leu Trp  
1715 1720 1725

Gln Gln His Ser Ile Thr Glu Glu Ile Gly His Ala Gln Glu Ala Asn  
1730 1735 1740

Gln Thr Leu Val Gly Ile Asp Trp Gln His Leu  
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21

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24

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23

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23

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18

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23

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23

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<223> Description of Artificial Sequence: Primer 2385-94

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20

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Val Asp Phe Tyr Thr Ala Phe Leu His His Leu Ala Gln Leu Val Pro  
35 40 45  
Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu Glu Lys Gln Glu Glu  
50 55 60  
Ser Val Gln Met Ser Ile Leu Thr Pro Leu Glu Trp Tyr Leu Phe Gly  
65 70 75 80  
Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys His Ser Gly Ala Phe  
85 90 95  
Gln Leu Cys Gly Lys Val Phe Lys Ser Gly Glu Thr Thr Tyr Ser Cys  
100 105 110  
Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu Cys Met Asp Cys Phe  
115 120 125  
Gln Ser Ser Val His Lys Asn His Arg Tyr Lys Met His Thr Ser Thr  
130 135 140  
Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Thr Gly  
145 150 155 160  
Pro Phe Cys Val Asp His Glu Pro Gly Arg Ala Gly Thr Thr Lys Glu  
165 170 175  
Ser Leu His Cys Pro Leu Asn Glu Glu Val Ile Ala Gln Ala Arg Arg  
180 185 190  
Ile Phe Pro Ser Val Ile Lys Tyr Ile Val Glu Met Thr Ile Trp Glu  
195 200 205  
Glu Glu Lys Glu Leu Pro Pro Glu Leu Gln Ile Arg Glu Lys Asn Glu  
210 215 220  
Arg Tyr Tyr Cys Val Leu Phe Asn Asp Glu His His Ser Tyr Asp His  
225 230 235 240  
Val Ile Tyr Ser Leu Gln Arg Ala Leu Asp Cys Glu Leu Ala Glu Ala  
245 250 255  
Gln Leu His Thr Thr Ala Ile Asp Lys Glu Gly Arg Arg Ala Val Lys  
260 265 270  
Ala Gly Val Tyr Ala Thr Cys Gln Glu Ala Lys Glu Asp Ile Lys Ser  
275 280 285  
His Ser Glu Asn Val Ser Gln His Pro Leu His Val Glu Val Leu His  
290 295 300  
Ser Val Val Met Ala His Gln Lys Phe Ala Leu Arg Leu Gly Ser Trp  
305 310 315 320  
Met Asn Lys Ile Met Ser Tyr Ser Ser Asp Phe Arg Gln Ile Phe Cys  
325 330 335

Gln Ala Cys Leu Val Glu Glu Pro Gly Ser Glu Asn Pro Cys Leu Ile  
 340 345 350  
 Ser Arg Leu Met Leu Trp Asp Ala Lys Leu Tyr Lys Gly Ala Arg Lys  
 355 360 365  
 Ile Leu His Glu Leu Ile Phe Ser Ser Phe Phe Met Glu Met Glu Tyr  
 370 375 380  
 Lys Lys Leu Phe Ala Met Glu Phe Val Lys Tyr Tyr Lys Gln Leu Gln  
 385 390 395 400  
 Lys Glu Tyr Ile Ser Asp Asp His Glu Arg Ser Ile Ser Ile Thr Ala  
 405 410 415  
 Leu Ser Val Gln Met Leu Thr Val Pro Thr Leu Ala Arg His Leu Ile  
 420 425 430  
 Glu Glu Gln Asn Val Ile Ser Val Ile Thr Glu Thr Leu Leu Glu Val  
 435 440 445  
 Leu Pro Glu Tyr Leu Asp Arg Asn Asn Lys Phe Asn Phe Gln Gly Tyr  
 450 455 460  
 Ser Gln Asp Lys Leu Gly Arg Val Tyr Ala Val Ile Cys Asp Leu Lys  
 465 470 475 480  
 Tyr Ile Leu Ile Ser Lys Pro Val Ile Trp Thr Glu Arg Leu Arg Ala  
 485 490 495  
 Gln Phe Leu Glu Gly Phe Arg Ser Phe Leu Lys Ile Leu Thr Cys Met  
 500 505 510  
 Gln Gly Met Glu Glu Ile Arg Arg Gln Val Gly Gln His Ile Glu Val  
 515 520 525  
 Asp Pro Asp Trp Glu Ala Ala Ile Ala Ile Gln Met Gln Leu Lys Asn  
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 Ile Leu Leu Met Phe Gln Glu Trp Cys Ala Cys Asp Glu Asp Leu Leu  
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 Leu Val Ala Tyr Lys Glu Cys His Lys Ala Val Met Arg Cys Ser Thr  
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 Asn Phe Met Ser Ser Thr Lys Thr Val Val Gln Leu Cys Gly His Ser  
 580 585 590  
 Leu Glu Thr Lys Ser Tyr Lys Val Ser Glu Asp Leu Val Ser Ile His  
 595 600 605  
 Leu Pro Leu Ser Arg Thr Leu Ala Gly Leu His Val Arg Leu Ser Arg  
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 625 630 635 640  
 Gln Val Glu Val Leu Val Glu Tyr Pro Leu Arg Cys Leu Val Leu Val  
 645 650 655  
 Ala Gln Val Val Ala Glu Met Trp Arg Arg Asn Gly Leu Ser Leu Ile  
 660 665 670

Ser	Gln	Val	Phe	Tyr	Tyr	Gln	Asp	Val	Lys	Cys	Arg	Glu	Glu	Met	Tyr		
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Asp	Lys	Asp	Ile	Ile	Met	Leu	Gln	Ile	Gly	Ala	Ser	Ile	Met	Asp	Pro		
		690					695					700					
Asn	Lys	Phe	Leu	Leu	Leu	Val	Leu	Gln	Arg	Tyr	Glu	Leu	Thr	Asp	Ala		
					710					715					720		
Phe	Asn	Lys	Thr	Ile	Ser	Thr	Lys	Asp	Gln	Asp	Leu	Ile	Lys	Gln	Tyr		
				725					730						735		
Asn	Thr	Leu	Ile	Glu	Glu	Met	Leu	Gln	Val	Leu	Ile	Tyr	Ile	Val	Gly		
			740						745					750			
Glu	Arg	Tyr	Val	Pro	Gly	Val	Gly	Asn	Val	Thr	Arg	Glu	Glu	Val	Ile		
		755					760							765			
Met	Arg	Glu	Ile	Thr	His	Leu	Leu	Cys	Ile	Glu	Pro	Met	Pro	His	Ser		
		770					775							780			
Ala	Ile	Ala	Arg	Asn	Leu	Pro	Glu	Asn	Glu	Asn	Asn	Glu	Thr	Gly	Leu		
		785				790				795					800		
Glu	Asn	Val	Ile	Asn	Lys	Val	Ala	Thr	Phe	Lys	Lys	Pro	Gly	Val	Ser		
				805					810						815		
Gly	His	Gly	Val	Tyr	Glu	Leu	Lys	Asp	Glu	Ser	Leu	Lys	Asp	Phe	Asn		
			820					825						830			
Met	Tyr	Phe	Tyr	His	Tyr	Ser	Lys	Thr	Gln	His	Ser	Lys	Ala	Glu	His		
		835					840						845				
Met	Gln	Lys	Lys	Arg	Arg	Lys	Gln	Glu	Asn	Lys	Asp	Glu	Ala	Leu	Pro		
		850				855					860						
Pro	Pro	Pro	Pro	Pro	Glu	Phe	Cys	Pro	Ala	Phe	Ser	Lys	Val	Val	Asn		
					870					875					880		
Leu	Leu	Ser	Cys	Asp	Val	Met	Ile	Tyr	Ile	Leu	Arg	Thr	Ile	Phe	Glu		
				885					890						895		
Arg	Ala	Val	Asp	Thr	Glu	Ser	Asn	Leu	Trp	Thr	Glu	Gly	Met	Leu	Gln		
			900					905						910			
Met	Ala	Phe	His	Ile	Leu	Ala	Leu	Gly	Leu	Leu	Glu	Glu	Lys	Gln	Gln		
		915					920					925					
Leu	Gln	Lys	Ala	Pro	Glu	Glu	Glu	Val	Ala	Phe	Asp	Phe	Tyr	His	Lys		
		930					935				940						
Ala	Ser	Arg	Leu	Gly	Ser	Ser	Ala	Met	Asn	Ala	Gln	Asn	Ile	Gln	Met		
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Leu	Leu	Glu	Arg	Leu	Lys	Gly	Ile	Pro	Gln	Leu	Glu	Gly	Gln	Lys	Asp		
				965					970						975		
Met	Ile	Thr	Trp	Ile	Leu	Gln	Met	Phe	Asp	Thr	Val	Lys	Arg	Leu	Arg		
			980					985					990				
Glu	Lys	Ser	Cys	Leu	Val	Val	Ala	Thr	Thr	Ser	Gly	Leu	Glu	Cys	Ile		
		995					1000						1005				

Lys Ser Glu Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg Lys Arg  
 1010 1015 1020  
 Lys Ala Glu Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala Gln Met  
 1025 1030 1035 1040  
 Ser Ala Leu Gln Lys Asn Phe Ile Glu Thr His Lys Leu Met Tyr Asp  
 1045 1050 1055  
 Asn Thr Ser Glu Val Thr Gly Lys Glu Asp Ser Ile Met Glu Glu Glu  
 1060 1065 1070  
 Ser Thr Ser Ala Val Ser Glu Ala Ser Arg Ile Ala Leu Gly Pro Lys  
 1075 1080 1085  
 Arg Gly Pro Ala Val Thr Glu Lys Glu Val Leu Thr Cys Ile Leu Cys  
 1090 1095 1100  
 Gln Glu Glu Gln Glu Val Lys Leu Glu Asn Asn Ala Met Val Leu Ser  
 1105 1110 1115 1120  
 Ala Cys Val Gln Lys Ser Thr Ala Leu Thr Gln His Arg Gly Lys Pro  
 1125 1130 1135  
 Val Asp His Leu Gly Glu Thr Leu Asp Pro Leu Phe Met Asp Pro Asp  
 1140 1145 1150  
 Leu Ala His Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met His Ala  
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 Arg Ile His Val Asp Leu Phe Asp Leu Glu Ser Gly Glu Tyr Leu Cys  
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 Pro Leu Cys Lys Ser Leu Cys Asn Thr Val Ile Pro Ile Ile Pro Leu  
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 Gln Pro Gln Lys Ile Asn Ser Glu Asn Ala Glu Ala Leu Ala Gln Leu  
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 Leu Thr Leu Ala Arg Trp Ile Gln Thr Val Leu Ala Arg Ile Ser Gly  
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 1285 1290 1295  
 Met Val Ile Leu Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys Val  
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 Pro Pro Asp Glu Leu Asp Pro Arg Val Pro Met Met Thr Trp Ser Thr  
 1315 1320 1325  
 Cys Ala Phe Thr Ile Gln Ala Ile Glu Asn Leu Leu Gly Asp Glu Gly  
 1330 1335 1340

Lys Pro Leu Phe Gly Ala Leu Gln Asn Arg Gln His Ser Gly Leu Lys  
 1345 1350 1355 1360  
 Ala Leu Met Gln Phe Ala Val Ala Gln Arg Ala Thr Cys Pro Gln Val  
 1365 1370 1375  
 Leu Ile His Lys His Leu Ala Arg Leu Leu Ser Val Ile Leu Pro Asn  
 1380 1385 1390  
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 Val Leu Val Gly Ala Val Leu Ala Phe Pro Ser Leu Tyr Trp Asp Asp  
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 Thr Val Asp Leu Gln Pro Ser Pro Leu Ser Ser Ser Tyr Asn His Leu  
 1425 1430 1435 1440  
 Tyr Leu Phe His Leu Ile Thr Met Ala His Met Leu Gln Ile Leu Leu  
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 Thr Thr Asp Thr Asp Leu Ser Pro Gly Pro Pro Leu Ala Glu Gly Glu  
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 Ser Gln His Thr Asp Gly Leu Thr Gly Cys Gly Ala Pro Gly Trp Tyr  
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 Ala Leu Leu Phe His Tyr Leu Leu Gly Val Ala Pro Pro Glu Glu Leu  
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 Ser Leu Pro Thr Asn Leu Phe Leu Leu Phe Gln Glu Tyr Trp Asp Thr  
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 Ser Leu Lys Gln Lys Ser Ala Val Val Arg Tyr Pro Arg Lys Arg Asn  
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 Ser Leu Ile Glu Leu Pro Glu Asp Tyr Ser Cys Leu Leu Asn Gln Ala  
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 Ser His Phe Arg Cys Pro Arg Ser Ala Asp Asp Glu Arg Lys His Pro  
 1620 1625 1630  
 Val Leu Cys Leu Phe Cys Gly Ala Ile Leu Cys Ser Gln Asn Ile Cys  
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 Cys Gln Glu Ile Val Asn Gly Glu Glu Val Gly Ala Cys Val Phe His  
 1650 1655 1660  
 Ala Leu His Cys Gly Ala Gly Val Cys Ile Phe Leu Lys Ile Arg Glu  
 1665 1670 1675 1680

Cys Arg Val Val Leu Val Glu Gly Lys Ala Arg Gly Cys Ala Tyr Pro  
                   1685                                  1690                                  1695  
 Ala Pro Tyr Leu Asp Glu Tyr Gly Glu Thr Asp Pro Gly Leu Lys Arg  
                   1700                                  1705                                  1710  
 Gly Asn Pro Leu His Leu Ser Arg Glu Arg Tyr Arg Lys Leu His Leu  
                   1715                                  1720                                  1725  
 Val Trp Gln Gln His Cys Ile Ile Glu Glu Ile Ala Arg Ser Gln Glu  
                   1730                                  1735                                  1740  
 Thr Asn Gln Met Leu Phe Gly Phe Asn Trp Gln Leu Leu  
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 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: peptide

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<210> 17  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: peptide

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<210> 18  
 <211> 5205  
 <212> DNA  
 <213> Homo sapiens

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 catcatttgg cacaattggt gccagaaatt tactttgctg aaatggaccc agacttggaa 180  
 aagcaggagg aaagtgtaca aatgtcaata ttactccac tggaatggta cttatttggg 240  
 gaagatccag atatttgctt agagaaattg aagcacagtg gagcatttca gctttgtggg 300  
 agggttttca aaagtggaga gacaacctat tcttgcaggg attgtgcaat tgatccaaca 360  
 tgtgtactct gtatggactg cttccaggac agtgttcata aaaatcatcg ttacaagatg 420  
 cataattcta ctggaggagg gttctgtgac tgtggagaca cagaggcatg gaaaactggc 480

cctttttgtg taaatcatga acctggaaga gcaggtacta taaaagagaa ttcacgctgt 540  
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gtcgtagaaa tgactatatg ggaagaggaa aaagaactgc ctctgaact ccagataagg 660  
knryycvndh hsydhgtcat atacagccta caaagagctc ttgactgtga gctcgcagag 720  
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tatgctgctt gccaggaagc aaaggaagat ataaagagtc attcagaaaa tgtctctcaa 840  
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tgccaagcat gccttagaga agaacctgac tcggagaatc cctgtctcat aagcagggtta 1020  
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aatgaaactg gcttagagaa tgtcataaac aaagtggcca catttaagaa accagggtgt 2400



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 cggaagctcc atttggtctg gcaacaacac tgcattatag aagagattgc taggagccaa 5160  
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 <211> 1735  
 <212> PRT  
 <213> Homo sapiens

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 Trp Trp Asp Gln Gln Val Asp Phe Tyr Thr Ala Phe Leu His His Leu  
 35 40 45  
 Ala Gln Leu Val Pro Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu  
 50 55 60  
 Glu Lys Gln Glu Glu Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu  
 65 70 75 80  
 Trp Tyr Leu Phe Gly Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys  
 85 90 95  
 His Ser Gly Ala Phe Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu  
 100 105 110  
 Thr Thr Tyr Ser Cys Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu  
 115 120 125  
 Cys Met Asp Cys Phe Gln Asp Ser Val His Lys Asn His Arg Tyr Lys  
 130 135 140

Met	His	Thr	Ser	Thr	Gly	Gly	Gly	Phe	Cys	Asp	Cys	Gly	Asp	Thr	Glu	145	150	155	160
Ala	Trp	Lys	Thr	Gly	Pro	Phe	Cys	Val	Asn	His	Glu	Pro	Gly	Arg	Ala	165	170		175
Gly	Thr	Ile	Lys	Glu	Asn	Ser	Arg	Cys	Pro	Leu	Asn	Glu	Glu	Val	Ile	180	185		190
Val	Gln	Ala	Arg	Lys	Ile	Phe	Pro	Ser	Val	Ile	Lys	Tyr	Val	Val	Glu	195	200	205	
Met	Thr	Ile	Trp	Glu	Glu	Glu	Lys	Glu	Leu	Pro	Pro	Glu	Leu	Gln	Ile	210	215	220	
Arg	Glu	Lys	Asn	Glu	Arg	Tyr	Tyr	Cys	Val	Leu	Phe	Asn	Asp	Glu	His	225	230	235	240
His	Ser	Tyr	Asp	His	Val	Ile	Tyr	Ser	Leu	Gln	Arg	Ala	Leu	Asp	Cys	245	250		255
Glu	Leu	Ala	Glu	Ala	Gln	Leu	His	Thr	Thr	Ala	Ile	Asp	Lys	Glu	Gly	260	265		270
Arg	Arg	Ala	Val	Lys	Ala	Gly	Ala	Tyr	Ala	Ala	Cys	Gln	Glu	Ala	Lys	275	280	285	
Glu	Asp	Ile	Lys	Ser	His	Ser	Glu	Asn	Val	Ser	Gln	His	Pro	Leu	His	290	295	300	
Val	Glu	Val	Leu	His	Ser	Glu	Ile	Met	Ala	His	Gln	Lys	Phe	Ala	Leu	305	310	315	320
Arg	Leu	Gly	Ser	Trp	Met	Asn	Lys	Ile	Met	Ser	Tyr	Ser	Ser	Asp	Phe	325	330		335
Arg	Gln	Ile	Phe	Cys	Gln	Ala	Cys	Leu	Arg	Glu	Glu	Pro	Asp	Ser	Glu	340	345	350	
Asn	Pro	Cys	Leu	Ile	Ser	Arg	Leu	Met	Leu	Trp	Asp	Ala	Lys	Leu	Tyr	355	360	365	
Lys	Gly	Ala	Arg	Lys	Ile	Leu	His	Glu	Leu	Ile	Phe	Ser	Ser	Phe	Phe	370	375	380	
Met	Glu	Met	Glu	Tyr	Lys	Lys	Leu	Phe	Ala	Met	Glu	Phe	Val	Lys	Tyr	385	390	395	400
Tyr	Lys	Gln	Leu	Gln	Lys	Glu	Tyr	Ile	Ser	Asp	Asp	His	Asp	Arg	Ser	405	410		415
Ile	Ser	Ile	Thr	Ala	Leu	Ser	Val	Gln	Met	Phe	Thr	Val	Pro	Thr	Leu	420	425	430	
Ala	Arg	His	Leu	Ile	Glu	Glu	Gln	Asn	Val	Ile	Ser	Val	Ile	Thr	Glu	435	440	445	
Thr	Leu	Leu	Glu	Val	Leu	Pro	Glu	Tyr	Leu	Asp	Arg	Asn	Asn	Lys	Phe	450	455	460	
Asn	Phe	Gln	Gly	Tyr	Ser	Gln	Asp	Lys	Leu	Gly	Arg	Val	Tyr	Ala	Val	465	470	475	480

Ile	Cys	Asp	Leu	Lys	Tyr	Ile	Leu	Ile	Ser	Lys	Pro	Thr	Ile	Trp	Thr		
				485					490					495			
Glu	Arg	Leu	Arg	Met	Gln	Phe	Leu	Glu	Gly	Phe	Arg	Ser	Phe	Leu	Lys		
				500				505					510				
Ile	Leu	Thr	Cys	Met	Gln	Gly	Met	Glu	Glu	Ile	Arg	Arg	Gln	Val	Gly		
		515					520					525					
Gln	His	Ile	Glu	Val	Asp	Pro	Asp	Trp	Glu	Ala	Ala	Ile	Ala	Ile	Gln		
		530				535					540						
Met	Gln	Leu	Lys	Asn	Ile	Leu	Leu	Met	Phe	Gln	Glu	Trp	Cys	Ala	Cys		
545				550					555						560		
Asp	Glu	Glu	Leu	Leu	Leu	Val	Ala	Tyr	Lys	Glu	Cys	His	Lys	Ala	Val		
				565					570					575			
Met	Arg	Cys	Ser	Thr	Ser	Phe	Ile	Ser	Ser	Ser	Lys	Thr	Val	Val	Gln		
			580					585					590				
Ser	Cys	Gly	His	Ser	Leu	Glu	Thr	Lys	Ser	Tyr	Arg	Val	Ser	Glu	Asp		
		595					600					605					
Leu	Val	Ser	Ile	His	Leu	Pro	Leu	Ser	Arg	Thr	Leu	Ala	Gly	Leu	His		
		610				615					620						
Val	Arg	Leu	Ser	Arg	Leu	Gly	Ala	Val	Ser	Arg	Leu	His	Glu	Phe	Val		
625					630					635					640		
Ser	Phe	Glu	Asp	Phe	Gln	Val	Glu	Val	Leu	Val	Glu	Tyr	Pro	Leu	Arg		
				645					650					655			
Cys	Leu	Val	Leu	Val	Ala	Gln	Val	Val	Ala	Glu	Met	Trp	Arg	Arg	Asn		
			660					665					670				
Gly	Leu	Ser	Leu	Ile	Ser	Gln	Val	Phe	Tyr	Tyr	Gln	Asp	Val	Lys	Cys		
		675					680					685					
Arg	Glu	Glu	Met	Tyr	Asp	Lys	Asp	Ile	Ile	Met	Leu	Gln	Ile	Gly	Ala		
		690				695					700						
Ser	Leu	Met	Asp	Pro	Asn	Lys	Phe	Leu	Leu	Leu	Val	Leu	Gln	Arg	Tyr		
705					710					715					720		
Glu	Leu	Ala	Glu	Ala	Phe	Asn	Lys	Thr	Ile	Ser	Thr	Lys	Asp	Gln	Asp		
				725					730					735			
Leu	Ile	Lys	Gln	Tyr	Asn	Thr	Leu	Ile	Glu	Glu	Met	Leu	Gln	Val	Leu		
			740					745					750				
Ile	Tyr	Ile	Val	Gly	Glu	Arg	Tyr	Val	Pro	Gly	Val	Gly	Asn	Val	Thr		
		755					760					765					
Lys	Glu	Glu	Val	Thr	Met	Arg	Glu	Ile	Ile	His	Leu	Leu	Cys	Ile	Glu		
		770				775					780						
Pro	Met	Pro	His	Ser	Ala	Ile	Ala	Lys	Asn	Leu	Pro	Glu	Asn	Glu	Asn		
785					790					795					800		
Asn	Glu	Thr	Gly	Leu	Glu	Asn	Val	Ile	Asn	Lys	Val	Ala	Thr	Phe	Lys		
				805					810					815			

Lys Pro Gly Val Ser Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser  
 820 825 830  
 Leu Lys Asp Phe Asn Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His  
 835 840 845  
 Ser Lys Ala Glu His Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys  
 850 855 860  
 Asp Glu Ala Leu Pro Pro Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe  
 865 870 875 880  
 Ser Lys Val Ile Asn Leu Leu Asn Cys Asp Ile Met Met Tyr Ile Leu  
 885 890 895  
 Arg Thr Val Phe Glu Arg Ala Ile Asp Thr Asp Ser Asn Leu Trp Thr  
 900 905 910  
 Glu Gly Met Leu Gln Met Ala Phe His Ile Leu Ala Leu Gly Leu Leu  
 915 920 925  
 Glu Glu Lys Gln Gln Leu Gln Lys Ala Pro Glu Glu Glu Val Thr Phe  
 930 935 940  
 Asp Phe Tyr His Lys Ala Ser Arg Leu Gly Ser Ser Ala Met Asn Ile  
 945 950 955 960  
 Gln Met Leu Leu Glu Lys Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln  
 965 970 975  
 Lys Asp Met Ile Thr Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg  
 980 985 990  
 Leu Arg Glu Lys Ser Cys Leu Ile Val Ala Thr Thr Ser Gly Ser Glu  
 995 1000 1005  
 Ser Ile Lys Asn Asp Glu Ile Thr His Asp Lys Glu Lys Ala Glu Arg  
 1010 1015 1020  
 Lys Arg Lys Ala Glu Ala Ala Arg Leu His Arg Gln Lys Ile Met Ala  
 1025 1030 1035 1040  
 Gln Met Ser Ala Leu Gln Lys Asn Phe Ile Glu Thr His Lys Leu Met  
 1045 1050 1055  
 Tyr Asp Asn Thr Ser Glu Met Pro Gly Lys Glu Asp Ser Ile Met Glu  
 1060 1065 1070  
 Glu Glu Ser Thr Pro Ala Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly  
 1075 1080 1085  
 Pro Lys Arg Gly Pro Ser Val Thr Glu Lys Glu Val Leu Thr Cys Ile  
 1090 1095 1100  
 Leu Cys Gln Glu Glu Gln Glu Val Lys Ile Glu Asn Asn Ala Met Val  
 1105 1110 1115 1120  
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 Lys Pro Ile Glu Leu Ser Gly Glu Ala Leu Asp Pro Leu Phe Met Asp  
 1140 1145 1150

Pro Asp Leu Ala Tyr Gly Thr Tyr Thr Gly Ser Cys Gly His Val Met  
 1155 1160 1165  
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 1250 1255 1260  
 Phe Phe Asn Gln Gly Met Gly Asp Ser Thr Leu Glu Phe His Ser Ile  
 1265 1270 1275 1280  
 Leu Ser Phe Gly Val Glu Ser Ser Ile Lys Tyr Ser Asn Ser Ile Lys  
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 Glu Met Val Ile Leu Phe Ala Thr Thr Ile Tyr Arg Ile Gly Leu Lys  
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